

[Sequence Listing]

SEQ ID No: 1

Length of Sequence: 1874

5

Type of Sequence: Nucleic Acid

Topology: Linear

Strandness: Double strands

Kinds of Sequence: cDNA to mRNA

Origin

10

Orgnism Name: Tobacco (*Nicotiana tabacum*)

Strain name: Xanthi NC

Character of Sequence

Sign designating character: CDS

Position that locates: 26..1672

15

Way of determining character: P

AGCGCGTCT ACAAGTCAGG CAGTC ATG ACA ACA ACT CCC ATC GCC AAT CAT 52

Met Thr Thr Thr Pro Ile Ala Asn His

20

1

5

CCT AAT ATT TTC ACT CAC CAG TCG TCG TCA TCG CCA TTG GCA TTC TTA 100

Pro Asn Ile Phe Thr His Gln Ser Ser Ser Ser Pro Leu Ala Phe Leu

10

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AAC CGT ACG AGT TTC ATC CCT TTC TCT TCA ATC TCC AAG CGC AAT AGT 148

Asn Arg Thr Ser Phe Ile Pro Phe Ser Ser Ile Ser Lys Arg Asn Ser

30

35

40

GTC AAT TGC AAT GGC TGG AGA ACA CGA TGC TCC GTT GCC AAA GAT TAC 196  
 Val Asn Cys Asn Gly Trp Arg Thr Arg Cys Ser Val Ala Lys Asp Tyr  
                   45                  50                  55

5 ACA GTT CCT TCC TCA GCG GTC GAC GGC GGA CCC GCC GCG GAG CTG GAC 244  
 Thr Val Pro Ser Ser Ala Val Asp Gly Gly Pro Ala Ala Glu Leu Asp  
                   60                  65                  70

TGT GTT ATA GTT GGA GCA GGA ATT AGT GGC CTC TGC ATT GCG CAG GTG 292  
 10 Cys Val Ile Val Gly Ala Gly Ile Ser Gly Leu Cys Ile Ala Gln Val  
                   75                  80                  85

ATG TCC GCT AAT TAC CCC AAT TTG ATG GTA ACC GAG GCG AGA GAT CGT 340  
 Met Ser Ala Asn Tyr Pro Asn Leu Met Val Thr Glu Ala Arg Asp Arg  
 15 90                  95                  100                  105

GCC GGT GGC AAC ATA ACG ACT GTG GAA AGA GAC GGC TAT TTG TGG GAA 388  
 Ala Gly Gly Asn Ile Thr Thr Val Glu Arg Asp Gly Tyr Leu Trp Glu  
                   110                  115                  120

20 GAA GGT CCC AAC AGT TTC CAG CCG TCC GAT CCT ATG TTG ACT ATG GCA 436  
 Glu Gly Pro Asn Ser Phe Gln Pro Ser Asp Pro Met Leu Thr Met Ala  
                   125                  130                  135

25 GTA GAT TGT GGA TTG AAG GAT GAT TTG GTG TTG GGA GAT CCT AAT GCG 484  
 Val Asp Cys Gly Leu Lys Asp Asp Leu Val Leu Gly Asp Pro Asn Ala  
                   140                  145                  150

CCC CGT TTC GTT TTG TGG AAG GGT AAA TTA AGG CCC GTC CCC TCA AAA 532

Pro Arg Phe Val Leu Trp Lys Gly Lys Leu Arg Pro Val Pro Ser Lys  
 155 160 165

CTC ACT GAT CTT CCC TTT TTT GAT TTG ATG AGC ATT CCT GGC AAG TTG 580  
 5 Leu Thr Asp Leu Pro Phe Phe Asp Leu Met Ser Ile Pro Gly Lys Leu  
 170 175 180 185

AGA GCT GGT TTT GGT GCC ATT GGC CTC CGC CCT TCA CCT CCA GGT CAT 628  
 Arg Ala Gly Phe Gly Ala Ile Gly Leu Arg Pro Ser Pro Pro Gly His  
 10 190 195 200

GAG GAA TCA GTT GAG CAG TTC GTG CGT CGT AAT CTT GGT GGC GAA GTC 676  
 Glu Glu Ser Val Glu Gln Phe Val Arg Arg Asn Leu Gly Gly Glu Val  
 205 210 215

15 TTT GAA CGC TTG ATA GAA CCA TTT TGT TCT GGT GTT TAT GCT GGT GAT 724  
 Phe Glu Arg Leu Ile Glu Pro Phe Cys Ser Gly Val Tyr Ala Gly Asp  
 220 225 230

20 CCC TCA AAA CTG AGT ATG AAA GCA GCA TTT GGG AAA GTT TGG AAG TTG 772  
 Pro Ser Lys Leu Ser Met Lys Ala Ala Phe Gly Lys Val Trp Lys Leu  
 235 240 245

GAA GAA ACT GGT GGT AGC ATT ATT GGA GGA ACC TTT AAA GCA ATA AAG 820  
 25 Glu Glu Thr Gly Gly Ser Ile Ile Gly Gly Thr Phe Lys Ala Ile Lys  
 250 255 260 265

GAG AGA TCC AGT ACA CCT AAA GCG CCC CGC GAT CCG CGT TTA CCT AAA 868  
 Glu Arg Ser Ser Thr Pro Lys Ala Pro Arg Asp Pro Arg Leu Pro Lys

	270	275	280	
	CCA AAA GGA CAG ACA GTT GGA TCA TTC AGG AAG GGT CTC AGA ATG CTG			916
	Pro Lys Gly Gln Thr Val Gly Ser Phe Arg Lys Gly Leu Arg Met Leu			
	285	290	295	
5				
	CCG GAT GCA ATC AGT GCA AGA TTG GGA AGC AAA TTA AAA CTA TCA TGG			964
	Pro Asp Ala Ile Ser Ala Arg Leu Gly Ser Lys Leu Lys Leu Ser Trp			
	300	305	310	
10				
	AAG CTT TCT AGC ATT ACT AAG TCA GAA AAA GGA GGA TAT CAC TTG ACA			1012
	Lys Leu Ser Ser Ile Thr Lys Ser Glu Lys Gly Gly Tyr His Leu Thr			
	315	320	325	
	TAC GAG ACA CCA GAA GGA GTA GTT TCT CTT CAA AGT CGA AGC ATT GTC			1060
15	Tyr Glu Thr Pro Glu Gly Val Val Ser Leu Gln Ser Arg Ser Ile Val			
	330	335	340	345
	ATG ACT GTG CCA TCC TAT GTA GCA AGC AAC ATA TTA CGT CCT CTT TCG			1108
	Met Thr Val Pro Ser Tyr Val Ala Ser Asn Ile Leu Arg Pro Leu Ser			
20		350	355	360
	GTT GCC GCA GCA GAT GCA CTT TCA AAT TTC TAC TAT CCC CCA GTT GGA			1156
	Val Ala Ala Ala Asp Ala Leu Ser Asn Phe Tyr Tyr Pro Pro Val Gly			
	365	370	375	
25				
	GCA GTC ACA ATT TCA TAT CCT CAA GAA GCT ATT CGT GAT GAG CGT CTG			1204
	Ala Val Thr Ile Ser Tyr Pro Gln Glu Ala Ile Arg Asp Glu Arg Leu			
	380	385	390	

GTT GAT GGT GAA CTA AAG GGA TTT GGG CAG TTG CAT CCA CGT ACA CAG 1252  
 Val Asp Gly Glu Leu Lys Gly Phe Gly Gln Leu His Pro Arg Thr Gln  
 395 400 405

5 GGA GTG GAA ACA CTA GGA ACG ATA TAT AGT TCA TCA CTC TTC CCT AAC 1300  
 Gly Val Glu Thr Leu Gly Thr Ile Tyr Ser Ser Ser Leu Phe Pro Asn  
 410 415 420 425

CGT GCC CCA AAA GGT CGG GTG CTA CTC TTG AAC TAC ATT GGA GGA GCA 1348  
 10 Arg Ala Pro Lys Gly Arg Val Leu Leu Leu Asn Tyr Ile Gly Gly Ala  
 430 435 440

AAA AAT CCT GAA ATT TTG TCT AAG ACG GAG AGC CAA CTT GTG GAA GTA 1396  
 Lys Asn Pro Glu Ile Leu Ser Lys Thr Glu Ser Gln Leu Val Glu Val  
 15 445 450 455

GTT GAT CGT GAC CTC AGA AAA ATG CTT ATA AAA CCC AAA GCT CAA GAT 1444  
 Val Asp Arg Asp Leu Arg Lys Met Leu Ile Lys Pro Lys Ala Gln Asp  
 460 465 470

20 CCT CTT GTT GTG GGT GTG CGA GTA TGG CCA CAA GCT ATC CCA CAG TTT 1492  
 Pro Leu Val Val Gly Val Arg Val Trp Pro Gln Ala Ile Pro Gln Phe  
 475 480 485

25 TTG GTT GGT CAT CTG GAT ACG CTA AGT ACT GCA AAA GCT GCT ATG AAT 1540  
 Leu Val Gly His Leu Asp Thr Leu Ser Thr Ala Lys Ala Ala Met Asn  
 490 495 500 505

GAT AAT GGG CTT GAA GGG CTG TTT CTT GGG GGT AAT TAT GTG TCA GGT 1588

Asp Asn Gly Leu Glu Gly Leu Phe Leu Gly Gly Asn Tyr Val Ser Gly  
 510 515 520

GTA GCA TTG GGG AGG TGT GTT GAA GGT GCT TAT GAA GTT GCA TCC GAG 1636  
 5 Val Ala Leu Gly Arg Cys Val Glu Gly Ala Tyr Glu Val Ala Ser Glu  
 525 530 535

GTA ACA GGA TTT CTG TCT CGG TAT GCA TAC AAA TGAAACCTGT GTTGGGGTA 1689  
 Val Thr Gly Phe Leu Ser Arg Tyr Ala Tyr Lys  
 10 540 545

GTCCAAACCT TGTTAGTAGT ACGATCATGC CTTGGGAAAA TTGGCATGTG CCTAAAAAGTT 1749  
 TTGCTCATTAGAGTATTATTT AGCCTTGGTA AATGATTGT ACTTGATATC AGTCGTTTTTC 1809  
 TTTGAGATAA AATGTTCTCG TTCAGGAAAT ATAATGTATA TCAATTTTAA AAAAAAAAAA 1869  
 AAAAA 1874

15

SEQ ID No.: 2

Length of Sequence: 548

Type of Sequence: Amino acid

Topology: Linear

5 Kind of Sequence: Protein

Origin:

Organism Name: Tobacco (*Nicotiana tabacum*)

Strain name: SR1

10

Met Thr Thr Thr Pro Ile Ala Asn His Pro Asn Ile Phe Thr His Gln  
1 5 10 15

Ser Ser Ser Ser Pro Leu Ala Phe Leu Asn Arg Thr Ser Phe Ile Pro  
15 20 25 30

Phe Ser Ser Ile Ser Lys Arg Asn Ser Val Asn Cys Asn Gly Trp Arg  
35 40 45

20 Thr Arg Cys Ser Val Ala Lys Asp Tyr Thr Val Pro Ser Ser Ala Val  
50 55 60

Asp Gly Gly Pro Ala Ala Glu Leu Asp Cys Val Ile Val Gly Ala Gly  
65 70 75 80

25

Ile Ser Gly Leu Cys Ile Ala Gln Val Met Ser Ala Asn Tyr Pro Asn  
85 90 95

Leu Met Val Thr Glu Ala Arg Asp Arg Ala Gly Gly Asn Ile Thr Thr

	100	105	110
	Val Glu Arg Asp Gly Tyr Leu Trp Glu Glu Gly Pro Asn Ser Phe Gln		
	115	120	125
5	Pro Ser Asp Pro Met Leu Thr Met Ala Val Asp Cys Gly Leu Lys Asp		
	130	135	140
	Asp Leu Val Leu Gly Asp Pro Asn Ala Pro Arg Phe Val Leu Trp Lys		
10	145	150	155 160
	Gly Lys Leu Arg Pro Val Pro Ser Lys Leu Thr Asp Leu Pro Phe Phe		
	165	170	175
15	Asp Leu Met Ser Ile Pro Gly Lys Leu Arg Ala Gly Phe Gly Ala Ile		
	180	185	190
	Gly Leu Arg Pro Ser Pro Pro Gly His Glu Glu Ser Val Glu Gln Phe		
	195	200	205
20	Val Arg Arg Asn Leu Gly Gly Glu Val Phe Glu Arg Leu Ile Glu Pro		
	210	215	220
	Phe Cys Ser Gly Val Tyr Val Gly Asp Pro Ser Lys Leu Ser Met Lys		
25	225	230	235 240
	Ala Ala Phe Gly Lys Val Trp Lys Leu Glu Glu Thr Gly Gly Ser Ile		
	245	250	255



Ile Gly Gly Thr Phe Lys Ala Ile Lys Glu Arg Ser Ser Thr Pro Lys  
 260 265 270

Ala Pro Arg Asp Pro Arg Leu Pro Lys Pro Lys Gly Gln Thr Val Gly  
 5 275 280 285

Ser Phe Arg Lys Gly Leu Arg Met Leu Pro Asp Ala Ile Ser Ala Arg  
 290 295 300

10 Leu Gly Ser Lys Leu Lys Leu Ser Trp Lys Leu Ser Ser Ile Thr Lys  
 305 310 315 320

Ser Glu Lys Gly Gly Tyr His Leu Thr Tyr Glu Thr Pro Glu Gly Val  
 325 330 335

15 Val Ser Leu Gln Ser Arg Ser Ile Val Met Thr Val Pro Ser Tyr Val  
 340 345 350

Ala Ser Asn Ile Leu Arg Pro Leu Ser Val Ala Ala Ala Asp Ala Leu  
 20 355 360 365

Ser Asn Phe Tyr Tyr Pro Pro Val Gly Ala Val Thr Ile Ser Tyr Pro  
 370 375 380

25 Gln Glu Ala Ile Arg Asp Glu Arg Leu Val Asp Gly Glu Leu Lys Gly  
 385 390 395 400

Phe Gly Gln Leu His Pro Arg Thr Gln Gly Val Glu Thr Leu Gly Thr  
 405 410 415

Ile Tyr Ser Ser Ser Leu Phe Pro Asn Arg Ala Pro Lys Gly Arg Val

420 425 430

5 Leu Leu Leu Asn Tyr Ile Gly Gly Ala Lys Asn Pro Glu Ile Leu Ser

435 440 445

Lys Thr Glu Ser Gln Leu Val Glu Val Val Asp Arg Asp Leu Arg Lys

450 455 460

10

Met Leu Ile Lys Pro Lys Ala Gln Asp Pro Leu Val Val Gly Val Arg

465 470 475 480

Val Trp Pro Gln Ala Ile Pro Gln Phe Leu Val Gly His Leu Asp Thr

15 485 490 495

Leu Ser Thr Ala Lys Ala Ala Met Asn Asp Asn Gly Leu Glu Gly Leu

500 505 510

20 Phe Leu Gly Gly Asn Tyr Val Ser Gly Val Ala Leu Gly Arg Cys Val

515 520 525

Glu Gly Ala Tyr Glu Val Ala Ser Glu Val Thr Gly Phe Leu Ser Arg

530 535 540

25

Tyr Ala Tyr Lys

545

SEQ ID No.: 3

Length of Sequence: 1874

type of Sequence: Nucleic acid

Topology: Linear

5 Strandness: Double strands

Kind of Sequence: cDNA to mRNA

Origin

Organism Name: tobacco (*Nicotiana tabacum*)

Strain Name: SR1

10 Character of Sequence

Signal designating Character: CDS

Location: 26..1672

way for determining Character: P

15

AGCGCGGTCT ACAAGTCAGG CAGTC ATG ACA ACA ACT CCC ATC GCC AAT CAT 52

Met Thr Thr Thr Pro Ile Ala Asn His

1

5

20

CCT AAT ATT TTC ACT CAC CAG TCG TCG TCA TCG CCA TTG GCA TTC TTA 100

Pro Asn Ile Phe Thr His Gln Ser Ser Ser Ser Pro Leu Ala Phe Leu

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25

25 AAC CGT ACG AGT TTC ATC CCT TTC TCT TCA ATC TCC AAG CGC AAT AGT 148

Asn Arg Thr Ser Phe Ile Pro Phe Ser Ser Ile Ser Lys Arg Asn Ser

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GTC AAT TGC AAT GGC TGG AGA ACA CGA TGC TCC GTT GCC AAA GAT TAC 196

Val Asn Cys Asn Gly Trp Arg Thr Arg Cys Ser Val Ala Lys Asp Tyr  
 45 50 55  
 ACA GTT CCT TCC TCA GCG GTC GAC GGC GGA CCC GCC GCG GAG CTG GAC 244  
 5 Thr Val Pro Ser Ser Ala Val Asp Gly Gly Pro Ala Ala Glu Leu Asp  
 60 65 70  
 TGT GTT ATA GTT GGA GCA GGA ATT AGT GGC CTC TGC ATT GCG CAG GTG 292  
 Cys Val Ile Val Gly Ala Gly Ile Ser Gly Leu Cys Ile Ala Gln Val  
 10 75 80 85  
 ATG TCC GCT AAT TAC CCC AAT TTG ATG GTA ACC GAG GCG AGA GAT CGT 340  
 Met Ser Ala Asn Tyr Pro Asn Leu Met Val Thr Glu Ala Arg Asp Arg  
 90 95 100 105  
 15 GCC GGT GGC AAC ATA ACG ACT GTG GAA AGA GAC GGC TAT TTG TGG GAA 388  
 Ala Gly Gly Asn Ile Thr Thr Val Glu Arg Asp Gly Tyr Leu Trp Glu  
 110 115 120  
 20 GAA GGT CCC AAC AGT TTC CAG CCG TCC GAT CCT ATG TTG ACT ATG GCA 436  
 Glu Gly Pro Asn Ser Phe Gln Pro Ser Asp Pro Met Leu Thr Met Ala  
 125 130 135  
 GTA GAT TGT GGA TTG AAG GAT GAT TTG GTG TTG GGA GAT CCT AAT GCG 484  
 25 Val Asp Cys Gly Leu Lys Asp Asp Leu Val Leu Gly Asp Pro Asn Ala  
 140 145 150  
 CCC CGT TTC GTT TTG TGG AAG GGT AAA TTA AGG CCC GTC CCC TCA AAA 532  
 Pro Arg Phe Val Leu Trp Lys Gly Lys Leu Arg Pro Val Pro Ser Lys

	155	160	165	
	CTC ACT GAT CTT CCC TTT TTT GAT TTG ATG AGC ATT CCT GGC AAG TTG			580
	Leu Thr Asp Leu Pro Phe Phe Asp Leu Met Ser Ile Pro Gly Lys Leu			
5	170	175	180	185
	AGA GCT GGT TTT GGT GCC ATT GGC CTC CGC CCT TCA CCT CCA GGT CAT			628
	Arg Ala Gly Phe Gly Ala Ile Gly Leu Arg Pro Ser Pro Pro Gly His			
	190	195	200	
10	GAG GAA TCA GTT GAG CAG TTC GTG CGT CGT AAT CTT GGT GGC GAA GTC			676
	Glu Glu Ser Val Glu Gln Phe Val Arg Arg Asn Leu Gly Gly Glu Val			
	205	210	215	
15	TTT GAA CGC TTG ATA GAA CCA TTT TGT TCT GGT GTT TAT GTT GGT GAT			724
	Phe Glu Arg Leu Ile Glu Pro Phe Cys Ser Gly Val Tyr Val Gly Asp			
	220	225	230	
	CCC TCA AAA CTG AGT ATG AAA GCA GCA TTT GGG AAA GTT TGG AAG TTG			772
20	Pro Ser Lys Leu Ser Met Lys Ala Ala Phe Gly Lys Val Trp Lys Leu			
	235	240	245	
	GAA GAA ACT GGT GGT AGC ATT ATT GGA GGA ACC TTT AAA GCA ATA AAG			820
	Glu Glu Thr Gly Gly Ser Ile Ile Gly Gly Thr Phe Lys Ala Ile Lys			
25	250	255	260	265
	GAG AGA TCC AGT ACA CCT AAA GCG CCC CGC GAT CCG CGT TTA CCT AAA			868
	Glu Arg Ser Ser Thr Pro Lys Ala Pro Arg Asp Pro Arg Leu Pro Lys			
	270	275	280	

CCA AAA GGA CAG ACA GTT GGA TCA TTC AGG AAG GGT CTC AGA ATG CTG 916  
 Pro Lys Gly Gln Thr Val Gly Ser Phe Arg Lys Gly Leu Arg Met Leu

285

290

295

5 CCG GAT GCA ATC AGT GCA AGA TTG GGA AGC AAA TTA AAA CTA TCA TGG 964  
 Pro Asp Ala Ile Ser Ala Arg Leu Gly Ser Lys Leu Lys Leu Ser Trp

300

305

310

AAG CTT TCT AGC ATT ACT AAG TCA GAA AAA GGA GGA TAT CAC TTG ACA 1012  
 10 Lys Leu Ser Ser Ile Thr Lys Ser Glu Lys Gly Gly Tyr His Leu Thr

315

320

325

TAC GAG ACA CCA GAA GGA GTA GTT TCT CTT CAA AGT CGA AGC ATT GTC 1060  
 Tyr Glu Thr Pro Glu Gly Val Val Ser Leu Gln Ser Arg Ser Ile Val

15

330

335

340

345

ATG ACT GTG CCA TCC TAT GTA GCA AGC AAC ATA TTA CGT CCT CTT TCG 1108  
 Met Thr Val Pro Ser Tyr Val Ala Ser Asn Ile Leu Arg Pro Leu Ser

350

355

360

20

GTT GCC GCA GCA GAT GCA CTT TCA AAT TTC TAC TAT CCC CCA GTT GGA 1156  
 Val Ala Ala Ala Asp Ala Leu Ser Asn Phe Tyr Tyr Pro Pro Val Gly

365

370

375

25 GCA GTC ACA ATT TCA TAT CCT CAA GAA GCT ATT CGT GAT GAG CGT CTG 1204  
 Ala Val Thr Ile Ser Tyr Pro Gln Glu Ala Ile Arg Asp Glu Arg Leu

380

385

390

GTT GAT GGT GAA CTA AAG GGA TTT GGG CAG TTG CAT CCA CGT ACA CAG 1252

Val Asp Gly Glu Leu Lys Gly Phe Gly Gln Leu His Pro Arg Thr Gln  
 395 400 405

5 GGA GTG GAA ACA CTA GGA ACG ATA TAT AGT TCA TCA CTC TTC CCT AAC 1300  
 Gly Val Glu Thr Leu Gly Thr Ile Tyr Ser Ser Ser Leu Phe Pro Asn  
 410 415 420 425

10 CGT GCC CCA AAA GGT CGG GTG CTA CTC TTG AAC TAC ATT GGA GGA GCA 1348  
 Arg Ala Pro Lys Gly Arg Val Leu Leu Leu Asn Tyr Ile Gly Gly Ala  
 430 435 440

15 AAA AAT CCT GAA ATT TTG TCT AAG ACG GAG AGC CAA CTT GTG GAA GTA 1396  
 Lys Asn Pro Glu Ile Leu Ser Lys Thr Glu Ser Gln Leu Val Glu Val  
 445 450 455

GTT GAT CGT GAC CTC AGA AAA ATG CTT ATA AAA CCC AAA GCT CAA GAT 1444  
 Val Asp Arg Asp Leu Arg Lys Met Leu Ile Lys Pro Lys Ala Gln Asp  
 460 465 470

20 CCT CTT GTT GTG GGT GTG CGA GTA TGG CCA CAA GCT ATC CCA CAG TTT 1492  
 Pro Leu Val Val Gly Val Arg Val Trp Pro Gln Ala Ile Pro Gln Phe  
 475 480 485

25 TTG GTT GGT CAT CTG GAT ACG CTA AGT ACT GCA AAA GCT GCT ATG AAT 1540  
 Leu Val Gly His Leu Asp Thr Leu Ser Thr Ala Lys Ala Ala Met Asn  
 490 495 500 505

GAT AAT GGG CTT GAA GGG CTG TTT CTT GGG GGT AAT TAT GTG TCA GGT 1588  
 Asp Asn Gly Leu Glu Gly Leu Phe Leu Gly Gly Asn Tyr Val Ser Gly

	510	515	520	
	GTA GCA TTG GGG AGG TGT GTT GAA GGT GCT TAT GAA GTT GCA TCC GAG			1636
	Val Ala Leu Gly Arg Cys Val Glu Gly Ala Tyr Glu Val Ala Ser Glu			
5	525	530	535	
	GTA ACA GGA TTT CTG TCT CGG TAT GCA TAC AAA TGAAACCTGT GTTGGGGGTA			1689
	Val Thr Gly Phe Leu Ser Arg Tyr Ala Tyr Lys			
	540	545		
10	GTCCAAACCT TGTTAGTAGT ACGATCATGC CTTGGGAAAA TTGGCATGTG CCTAAAAAGTT			1749
	TTGCTCATT A GAGTTATTTT AGCCTTGGA AATGATTTGT ACTTGATATC AGTCGTTTTC			1809
	TTTGAGATAA AATGTTCTG TTCAGGAAAT ATAATGTATA TCAATTTTAA AAAAAAAAAA			1869
	AAAAA			1874

15



SEQ ID No.: 4

Length of Sequence: 23

type of Sequence: Nucleic acid

Strandness: single strand

5

topology: straight

kind of Sequence: other nucleic acid synthetic oligonucleotide

ATTGGTGGCG ACGACTCCTG GAG

10

SEQ ID No.: 5

Length of Sequence: 24

Type of Sequence: Nucleic acid

Strandness: single strand

15

Topology: straight

Kind of Sequence: other nucleic acid synthetic oligonucleotide

CCAGACCAAC TGGTAATGGT AGCG

20

SEQ ID No.: 6

Length of Sequence: 24

Type of Sequence: Nucleic acid

Strandness: single strand

25

topology: straight

Kind of Sequence: other nucleic acid synthetic oligonucleotide

GCGGTCTACA AGTCAGGCAG TCAT

SEQ ID No. : 7

Length of Sequence : 31

Type of Sequence : Nucleic acid

5 Strandness : single strand

Topology : straight

Kind of Sequence : other nucleic acid synthetic oligonucleotide

CATGCCAATT TTCCAAGGC ATGATCGTAC T

10

SEQ ID No. : 8

Length of Sequence : 20

Type of Sequence : Nucleic acid

Strandness : single strand

15

Topology : straight

kind of Sequence : other nucleic acid synthetic oligonucleotide

GGTGTATG TTGGTATCC·

20

Sequence Listing 9

SEQ ID No.: 9

Length of Sequence: 27

Type of Sequence: Nucleic acid

5 Strandness: single strand

Topology: straight

Kind of Sequence: other nucleic acid synthetic oligonucleotide

CACAGATGGT TAGAGAGGCT TACGCAG

10

Sequence Listing 10

SEQ ID No.: 10

Length of Sequence: 27

15

Type of Sequence: Nucleic acid

Number of chain: single strand

Topology: straight

kind of Sequence: other nucleic acid synthetic oligonucleotide

20 TCATCGCAAG ACCGGCAACA GGATTCA